

FIGURE 1

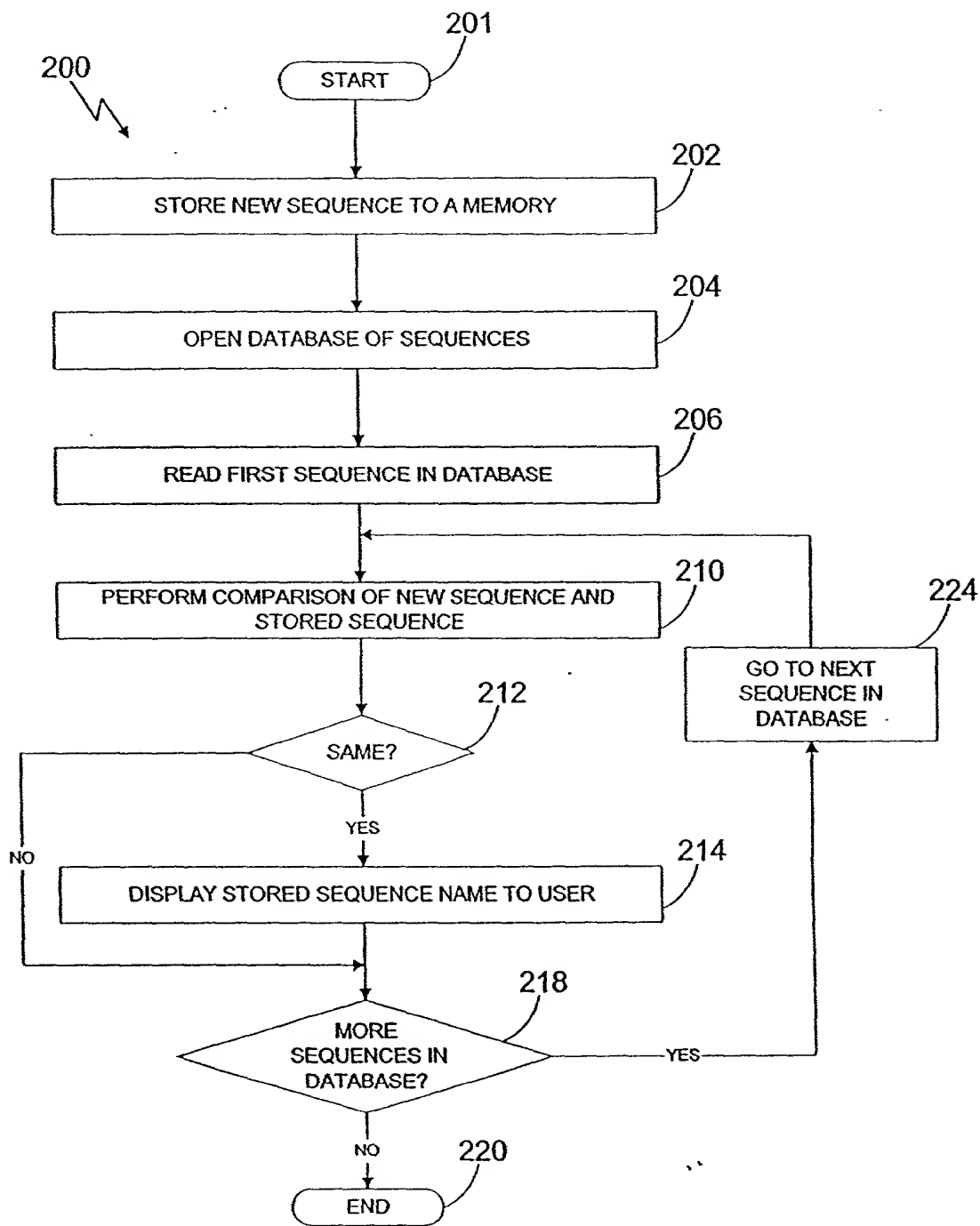


FIGURE 2

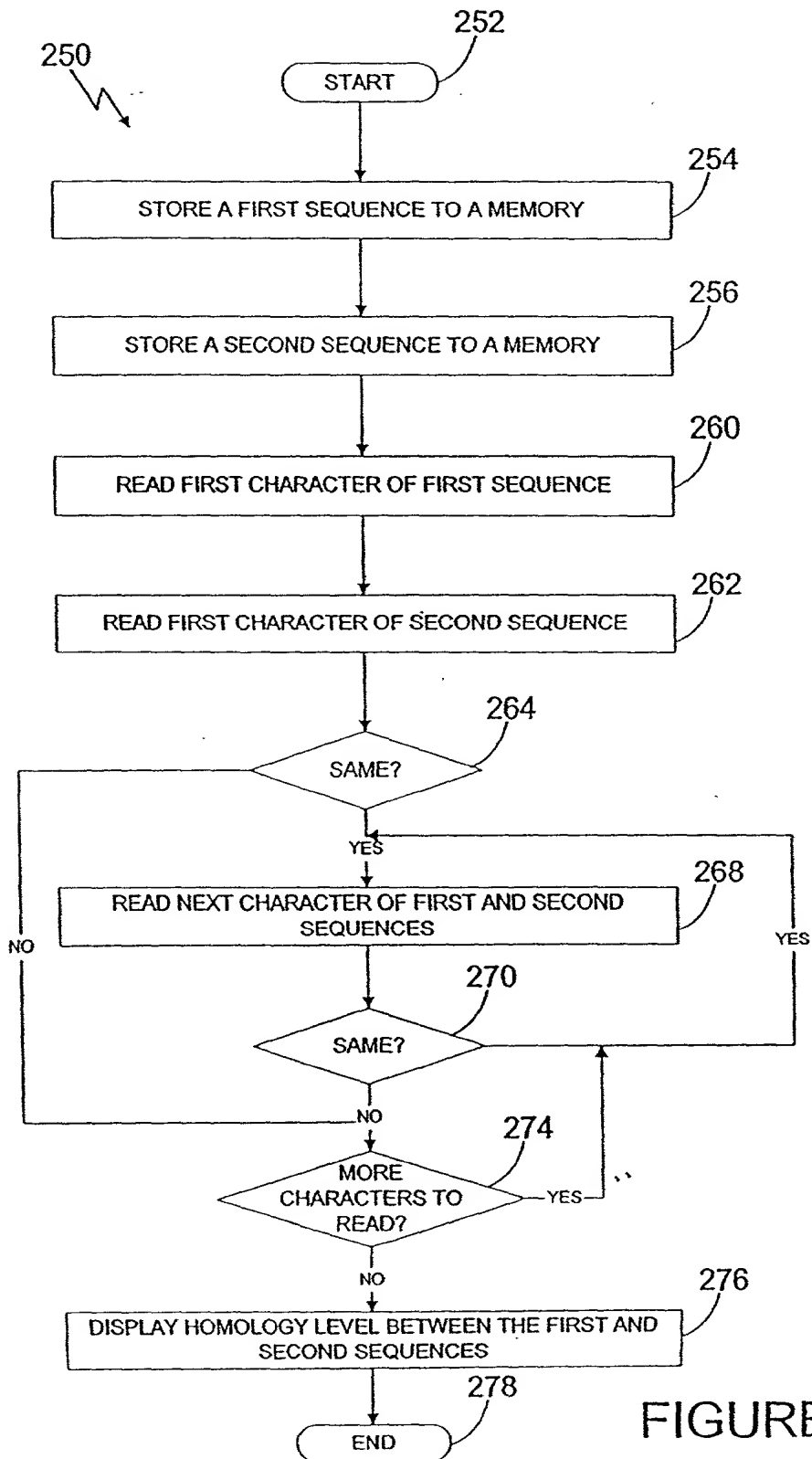
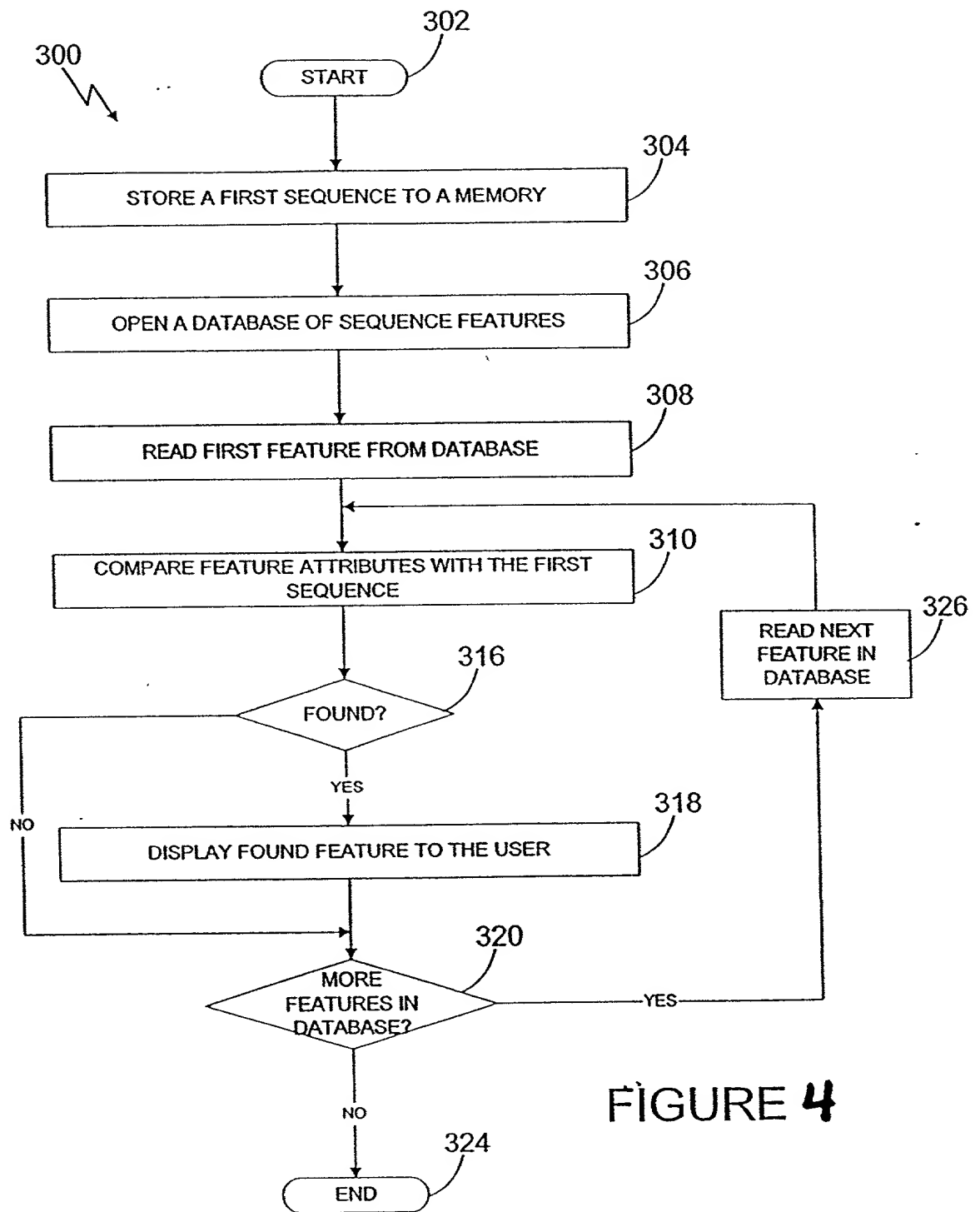


FIGURE 3



# FIGURE 5

*Ammonifex degensii* KC4 Phosphatase(3A1A=3A2A)  
Complete gene sequence

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1  ATGAGGGGGAGCGGAGTGC GGATACTTCTCACCAACGATGACGGCATCTTTGCCGAGGGT
   MetArgGlySerGlyValArgIleLeuLeuThrAsnAspAspGlyIlePheAlaGluGly

21 CTGGGGGCTCTGCGCAAGATGCTGGAGCCCGTGGCTACCCCTTTACGTGGTGGCTCCGGAC
   LeuGlyAlaLeuArgLysMetLeuGluProValAlaThrLeuTyrValValAlaProAsp

41 CGAGAGCGTAGCGCGGCCAGCCATGCTATCACCGTTACCGCCCCCTGCGGGTGCGGGAG
   ArgGluArgSerAlaAlaSerHisAlaIleThrValHisArgProLeuArgValArgGlu

61 GCGGGTTTTCGAGCCCCAGGCTTAAAGGCTGGGTAGTGGACGGTACCCCGCCGACTGC
   AlaGlyPheArgSerProArgLeuLysGlyTrpValValAspGlyThrProAlaAspCys

81 GTCAAGCTGGGCCTGGAGGTACTTTTGGCCGAACGTCCAGATTTCTGGTTTCGGGCATA
   ValLysLeuGlyLeuGluValLeuLeuProGluArgProAspPheLeuValSerGlyIle

101 AACTACGGGCCCCAACCTGGGTACCGACGTACTTTACTCCGGCACCGTCTCGGCGGCCATA
   AsnTyrGlyProAsnLeuGlyThrAspValLeuTyrSerGlyThrValSerAlaAlaIle

121 GAAGGGGTAATTAACGGCATTCCTCGGTGGCCGTATCTTTGGCCACGCGGCGGGAGCCG
   GluGlyValIleAsnGlyIleProSerValAlaValSerLeuAlaThrArgArgGluPro

141 GACTATACCTGGGCGGCCCCGGTTCGTCTCTGGTCTGCTGGAGGAACTGCGAAAAACACCAA
   AspTyrThrTrpAlaAlaArgPheValLeuValLeuLeuGluGluLeuArgLysHisGln

161 CTGCCCCCAGGAACCTGCTCAACGTCAACGTGCCCCGACGGGGTGCCCCGCGGGTCAAG
   LeuProProGlyThrLeuLeuAsnValAsnValProAspGlyValProArgGlyValLys

181 GTGACCAAACCTGGGAAGCGTACGCTACGTCAACGTGGTAGACTGCCGCACCGACCCCTCGG
   ValThrLysLeuGlySerValArgTyrValAsnValValAspCysArgThrAspProArg

201 GGGAAGGCTTACTACTGGATGGCGGGAGAACCATTTGGAGCTGGACGGCAACGACTCCGAA
   GlyLysAlaTyrTyrTrpMetAlaGlyGluProLeuGluLeuAspGlyAsnAspSerGlu

221 ACCGACGTCTGGGCGGTGCGAGAAGGCTATATTTCCGTAACACCGGTCCAGATCGACCTT
   ThrAspValTrpAlaValArgGluGlyTyrIleSerValThrProValGlnIleAspLeu

241 ACTAACTACGGCTTCTGGAAGAACTCAAAAAATGGCGTTTCAAGGATATCTTTTCTTCT
   ThrAsnTyrGlyPheLeuGluGluLeuLysLysTrpArgPheLysAspIlePheSerSer

TAA
261 End 261

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# FIGURE 6

## *Methanococcus igneus* K015 Phosphatase (9A1A) Complete Gene Sequence

ATGTTGGATATACTGCTTGTAAATGATGATGGCATTATTCAAATGGATTAAATAGCTTTG  
 1 MetLeuAspIleLeuLeuValAsnAspAspGlyIleTyrSerAsnGlyLeuIleAlaLeu  
 AAGGATGCATTATTGGAAAAATTTAATGCGAGGATTACTATTGTAGCCCCAACAAATCAG  
 21 LysAspAlaLeuLeuGluLysPheAsnAlaArgIleThrIleValAlaProThrAsnGln  
 CAGAGTGGTATTGGTAGGGCAATAAGTTTATTCGAGCCGTTAAGGATAACTAAAACCAAA  
 41 GlnSerGlyIleGlyArgAlaIleSerLeuPheGluProLeuArgIleThrLysThrLys  
 TTAGCAGATGGTTCTTGGGGATATGCAGTTTCAGGAACCCCAACAGATTGCGTTATATTG  
 61 LeuAlaAspGlySerTrpGlyTyrAlaValSerGlyThrProThrAspCysValIleLeu  
 GGCATTATGAGATATTAAAGAAGGTACCTGATGTAGTTATATCAGGAATAAACATTGGA  
 81 GlyIleTyrGluIleLeuLysLysValProAspValValIleSerGlyIleAsnIleGly  
 GAAACCTTGGGACTGAAATAACAACCTTCTGGAACGTTGGGGGCTGCGTTTGAAGGGGCC  
 101 GluAsnLeuGlyThrGluIleThrThrSerGlyThrLeuGlyAlaAlaPheGluGlyAla  
 CATCATGGGGCTAAGGCATTAGCATCATCACTCCAAGTTACCTCTGACCATCTAAAGTTT  
 121 HisHisGlyAlaLysAlaLeuAlaSerSerLeuGlnValThrSerAspHisLeuLysPhe  
 AAAGAGGGGGAGACCCCAATAGACTTCACAGTCCCAGCAAGAATTACTGCAAAATGTTGTT  
 141 LysGluGlyGluThrProIleAspPheThrValProAlaArgIleThrAlaAsnValVal  
 GAGAAGATGTTGGATTATGATTTCCCATGTGATGTCGTCAACTTAAACATTCCAGAAGGA  
 161 GluLysMetLeuAspTyrAspPheProCysAspValValAsnLeuAsnIleProGluGly  
 GCAACAGAAAAGACACCGATTGAAATCACAAGGTTGGCAAGGAAAATGTATACAACACAC  
 181 AlaThrGluLysThrProIleGluIleThrArgLeuAlaArgLysMetTyrThrThrHis  
 GTTGAGGAAAGAATAGATCCAAGAGGGAGGAGTTATTATTGGATTGATGGGTATCCTATT  
 201 ValGluGluArgIleAspProArgGlyArgSerTyrTyrTrpIleAspGlyTyrProIle  
 TTAGAGGAAGAGGAAGACACTGATGTCTATGTTGTTAGAAGAAAGGGACATATTTCTCTA  
 221 LeuGluGluGluGluAspThrAspValTyrValValArgArgLysGlyHisIleSerLeu  
 ACCCCATTAAACATTAGACACAACAATTAATAATTTAGAGGAATTTAAGAAAAAATATGAG  
 241 ThrProLeuThrLeuAspThrThrIleLysAsnLeuGluGluPheLysLysLysTyrGlu  
 AGAATATTAAATGAATGA  
 261 ArgIleLeuAsnGluEnd 266

# FIGURE 7

## *Thermococcus alcaliphilus* AEDII12RA Phosphatase (18A) Complete Gene Sequence

ATGATGATGGAATTCACCTCGCGAGGGAATAAAAGCTGCTGTAGAGGCACTTCAAGGGTTA  
 1 MetMetMetGluPheThrArgGluGlyIleLysAlaAlaValGluAlaLeuGlnGlyLeu  
 GGAGAGATCTACGTAGTTGCCCCAATGTTTCAAAGGAGCGCAAGTGAAGGGCAATGACC  
 21 GlyGluIleTyrValValAlaProMetPheGlnArgSerAlaSerGlyArgAlaMetThr  
 ATCCACAGACCTCTAAGGGCTAAAAGAATAAGTATGAACGGTGCAAAAGCAGCCTATGCT  
 41 IleHisArgProLeuArgAlaLysArgIleSerMetAsnGlyAlaLysAlaAlaTyrAla  
 TTGGATGGAATGCCCGTTGATTGCGTTATCTTTGCCATGGCCAGATTTGGAGATTTTCGAC  
 61 LeuAspGlyMetProValAspCysValIlePheAlaMetAlaArgPheGlyAspPheAsp  
 CTTGCAATAAGTGGTGTAACCTTGGGAGAAAACATGAGCACCGAGATAACGGTTTCCGGG  
 81 LeuAlaIleSerGlyValAsnLeuGlyGluAsnMetSerThrGluIleThrValSerGly  
 ACTGCAAGCGCTGCAATAGAGGCTGCAACCCAAGAGATCCCAAGCATTCCCATAAGCCTG  
 101 ThrAlaSerAlaAlaIleGluAlaAlaThrGlnGluIleProSerIleProIleSerLeu  
 GAAGTTAATAGAGAAAAACACAAATTTGGTGAGGGCGAAGAGATTGACTTCTCAGCTGCC  
 121 GluValAsnArgGluLysHisLysPheGlyGluGlyGluGluIleAspPheSerAlaAla  
 AAGTATTTCTTAAGAAAAATCGCAACGGCGGTTTTTAAAGAGAGGCCTCCCCAAAGGAGTC  
 141 LysTyrPheLeuArgLysIleAlaThrAlaValLeuLysArgGlyLeuProLysGlyVal  
 GATATGCTGAACGTCAACGTCCCTTATGATGCAAATGAAAGGACAGAGATAGCTTTTACT  
 161 AspMetLeuAsnValAsnValProTyrAspAlaAsnGluArgThrGluIleAlaPheThr  
 CGCCTGGCAAGAAGGATGTATAGGCCTTCTATTGAAGAGCGCATAGACCCAAAGGGGAAT  
 181 ArgLeuAlaArgArgMetTyrArgProSerIleGluGluArgIleAspProLysGlyAsn  
 CCCTACTACTGGATAGTTGGAACCTCAGTGCCCTAAGGAGGCATTAGAGCCGGGAACGGAT  
 201 ProTyrTyrTrpIleValGlyThrGlnCysProLysGluAlaLeuGluProGlyThrAsp  
 ATGTATGTAGTTAAAGTTGAGAGAAAAGTTAGCGTGACTCCAATAAACATTGATATGACA  
 221 MetTyrValValLysValGluArgLysValSerValThrProIleAsnIleAspMetThr  
 GCAAGAGTGAATTTAGACGAGATTAAAAGACTTTTAGAAGTGTAG  
 241 AlaArgValAsnLeuAspGluIleLysArgLeuLeuGluLeuEnd 255

# FIGURE 8

## *Thermococcus celer* Phosphatase (25A1A) Complete Gene Sequence

ATGAGAACCCTGACAATAAACACTGACGCGGAGGGGTTTCGTTTTGAGGATTCTCCTGACG  
 1 MetArgThrLeuThrIleAsnThrAspAlaGluGlyPheValLeuArgIleLeuLeuThr 20  
 AACGACGATGGAATCTACTCCAACGGACTGCGCGCCGCTGTGAAAGCCCTGAGTGAGCTC  
 21 AsnAspAspGlyIleTyrSerAsnGlyLeuArgAlaAlaValLysAlaLeuSerGluLeu 40  
 GGCGAAGTTTACGTCGTTGCCCCCTCTTCCAGAGGAGCGCGAGCGGCAGGGCCATGACG  
 41 GlyGluValTyrValValAlaProLeuPheGlnArgSerAlaSerGlyArgAlaMetThr 60  
 CTCCACAGGCCGATAAGGGCCAAGCGCGTTGACGTTCCCGGCGCAAAGATAGCCTACGGA  
 61 LeuHisArgProIleArgAlaLysArgValAspValProGlyAlaLysIleAlaTyrGly 80  
 ATAGATGGAACCTCTACTGACTGCGTGATTTTCGCCATAGCCCGCTTCGGGAGCTTTGGT  
 81 IleAspGlyThrProThrAspCysValIlePheAlaIleAlaArgPheGlySerPheGly 100  
 TTAGCCGTGAGCGGGATTAACTCGGCGAGAACCTGAGCACCGAGATAACAGTCTCAGGG  
 101 LeuAlaValSerGlyIleAsnLeuGlyGluAsnLeuSerThrGluIleThrValSerGly 120  
 ACGGCCTCCGCTGCCATAGAGGCCCTCAACTCATGGAATTCCGAGCATAGCGATTAGCCTT  
 121 ThrAlaSerAlaAlaIleGluAlaSerThrHisGlyIleProSerIleAlaIleSerLeu 140  
 GAGGTGGAGTGAAGAAGACCCCTCGGCGAGGGTGAGGGGGTTGACTTCTCGGTCTCGACT  
 141 GluValGluTrpLysLysThrLeuGlyGluGlyGluGlyValAspPheSerValSerThr 160  
 CACTTCCTCAAGAGAATCGCGGGAGCCCTCTTGGAGAGAGGTCTTCCTGAGGGCGTTGAC  
 161 HisPheLeuLysArgIleAlaGlyAlaLeuLeuGluArgGlyLeuProGluGlyValAsp 180  
 ATGCTCAACGTCAACGTTCCGAGCGACGCGACGGAGGAAACGGAGATAGCAATCACCCGC  
 181 MetLeuAsnValAsnValProSerAspAlaThrGluGluThrGluIleAlaIleThrArg 200  
 TTAGCCCGGAAGCGCTACTCCCCAACGGTCGAGGAGAGGATTGACCCCAAGGGCAACCCC  
 201 LeuAlaArgLysArgTyrSerProThrValGluGluArgIleAspProLysGlyAsnPro 220  
 TACTACTGGATTGTGCGCAAACCTTGTCCAAGACTTCGAGCCAGGGACAGATGCCTACGCC  
 221 TyrTyrTrpIleValGlyLysLeuValGlnAspPheGluProGlyThrAspAlaTyrAla 240  
 CTGAAGGTCGAGAGGAAGGTCAGCGTCACGCCGATAAACATAGATATGACTGCGAGGGTG  
 241 LeuLysValGluArgLysValSerValThrProIleAsnIleAspMetThrAlaArgVal 260  
 GACTTTGAGGAGCTTGTAAGGGTCTGTGGGTGTAA  
 261 AspPheGluGluLeuValArgValLeuTrpValEnd 272



# FIGURE 9A

## *Thermococcus* GU5L5 Phosphatase (26A1A) Complete Gene Sequence (Part 1 of 2)

ATGAAAGGAAAGTCTCTGTAGCGGTCTGTTGTTGGGTCTTTAATTTTGAGCCTGATT  
 1 MetLysGlyLysSerLeuValSerGlyLeuLeuLeuGlyLeuLeuIleLeuSerLeuIle 20  
 TCATTCAGCCAAGCTTTGCATACTCCCCACACGGCGGTGTCAAAAACATCATAATCCTG  
 21 SerPheGlnProSerPheAlaTyrSerProHisGlyGlyValLysAsnIleIleIleLeu 40  
 GTTGGAGACGGCATGGGTCTTGGGCATGTAGAAATTACAAAGCTCGTTTATGGACACTTA  
 41 ValGlyAspGlyMetGlyLeuGlyHisValGluIleThrLysLeuValTyrGlyHisLeu 60  
 AACATGGAAAACCTTCCAGTTACTGGATTTGAGCTTACTGATTCCCTAAGTGGTGAAGTT  
 61 AsnMetGluAsnPheProValThrGlyPheGluLeuThrAspSerLeuSerGlyGluVal 80  
 ACAGATTCTGCTGCGGCAGGAAC TGCAATATCCACTGGAGCTAAAACGTATAATGGTATG  
 81 ThrAspSerAlaAlaAlaGlyThrAlaIleSerThrGlyAlaLysThrTyrAsnGlyMet 100  
 ATTTTCAGTAACCAACATAACCGGAAAGATAGTTAACTTAACAACCCCTACTTGAAGTGGCT  
 101 IleSerValThrAsnIleThrGlyLysIleValAsnLeuThrThrLeuLeuGluValAla 120  
 CAAGAGCTTGGGAAGTCAACAGGGCTGGTCACCACAACAAGGATTACCCATGCAACTCCA  
 121 GlnGluLeuGlyLysSerThrGlyLeuValThrThrThrArgIleThrHisAlaThrPro 140  
 GCAGTTTTTTCGTCCTCCATGTCCCAGATAGGGATATGGAGGGGGAGATACCCAAGCAACTC  
 141 AlaValPheAlaSerHisValProAspArgAspMetGluGlyGluIleProLysGlnLeu 160  
 ATAATGCACAAAGTTAACGTCTTGTGGGTGGTGAAGGGAGAAATTCGATGAGAAAAAT  
 161 IleMetHisLysValAsnValLeuLeuGlyGlyGlyArgGluLysPheAspGluLysAsn 180  
 TTGGAGCTGGCCAAAAAGCAGGGATACAAAGTAGTTTTTCACGAAGGAAGAGCTTGAAAAA  
 181 LeuGluLeuAlaLysLysGlnGlyTyrLysValValPheThrLysGluGluLeuGluLys 200  
 GTTGAAGGAGATTATGTCCTAGGACTCTTTGCAGAAAGTCACATCCCTTACGTATTGGAT  
 201 ValGluGlyAspTyrValLeuGlyLeuPheAlaGluSerHisIleProTyrValLeuAsp 220  
 AGAAAACCCGATGATGTTGGACTTTTAGAAATGGCCAAAAGGCAATTTCAATACTCGAG  
 221 ArgLysProAspAspValGlyLeuLeuGluMetAlaLysLysAlaIleSerIleLeuGlu 240  
 AAGAACCCGAGCGGATTCTTTCTCATGGTTGAGGGCGGAAGGATTGACCATGCAGCCCAT  
 241 LysAsnProSerGlyPhePheLeuMetValGluGlyGlyArgIleAspHisAlaAlaHis 260  
 GGAAACGATGTCGCATCGGTGTTGTCAGAACTAAGGAGTTTGACGATGTTGTCAGATAC  
 261 GlyAsnAspValAlaSerValValAlaGluThrLysGluPheAspAspValValArgTyr 280  
 GTGCTGGAATATCCGAAGAAGAGGGGAGATACCTTGGTAATAGTGCTTGCCGATCACGAA  
 281 ValLeuGluTyrProLysLysArgGlyAspThrLeuValIleValLeuAlaAspHisGlu 300  
 ACTGGAGGTCTTGCAATAGGTCTAACGTATGGAAATGCAATCGATGAAGATGCCATAAGA  
 301 ThrGlyGlyLeuAlaIleGlyLeuThrTyrGlyAsnAlaIleAspGluAspAlaIleArg 320  
 AAAATAAAAGCAAGCACGTTGAGGATGCCCAAAGAGGTTAAGGCAGGAGTAGTGTA  
 321 LysIleLysAlaSerThrLeuArgMetProLysGluValLysAlaGlySerSerValLys 340

# FIGURE 90

## *Thermococcus* GU5L5 Phosphatase (26A1A) Complete Gene Sequence (Part 2 of 2)

341 GAGTCCTCAAAGGTATGCCGGATTTGTCCCAACAGAGGAAGAAGTCAGTATATTGAGAAT 360  
 GluSerSerLysValCysArgIleCysProAsnArgGlyArgSerGlnTyrIleGluAsn  
 361 GCGCTGCACTCGACAAACAAGTATGCCCTCTCAAATGCAGTAGCCGATGTTATAAACAGG 380  
 AlaLeuHisSerThrAsnLysTyrAlaLeuSerAsnAlaValAlaAspValIleAsnArg  
 381 CGTATTGGTGTGGATTACCTCCTATGAGCATACAGGAGTTCCAGTTCCGCTCTTAGCT 400  
 ArgIleGlyValGlyPheThrSerTyrGluHisThrGlyValProValProLeuLeuAla  
 401 TACGGTCCCGGGGCAGAGAACTTCAGAGGTTTCTTACACCATGTGGATACAGCAAGATTA 420  
 TyrGlyProGlyAlaGluAsnPheArgGlyPheLeuHisHisValAspThrAlaArgLeu  
 421 GTTGCAAAGTTAATGCTCTTTGGAAGGAGGAATATTCCAGTTACCATTTCAAGCGTGAGC 440  
 ValAlaLysLeuMetLeuPheGlyArgArgAsnIleProValThrIleSerSerValSer  
 441 AGTGTTAAGGGAGACATAACCGGTGATTACAGGGTTGATGAGAAGGATGCCTACGTTACG 460  
 SerValLysGlyAspIleThrGlyAspTyrArgValAspGluLysAspAlaTyrValThr  
 461 CTCATGATGTTTCTCGGAGAAAAAGTGGATAATGAAATTGAAAAGAGAGTCGATATAGAC 480  
 LeuMetMetPheLeuGlyGluLysValAspAsnGluIleGluLysArgValAspIleAsp  
 481 AACACGGCATGGTTGACTTAAATGACGTCATGTTGATTCTCCAGGAAGCTTGA 498  
 AsnAsnGlyMetValAspLeuAsnAspValMetLeuIleLeuGlnGluAlaEnd

# FIGURE 10A

## OC9a Phosphatase (27A3A) Complete Gene Sequence (Part 1 of 2)

ATGCCAAGAAATATCGCCGCTGTATGCGCCCTGGCCGCTTTGTTAGGGTCGGCCTGGGCG  
 1 MetProArgAsnIleAlaAlaValCysAlaLeuAlaAlaLeuLeuGlySerAlaTrpAla 20  
 GCCAAAGTTGCCGTCTACCCCTACGACGGAGCCGCTTTGCTGGCGGGGAGCGCTTCGAT  
 21 AlaLysValAlaValTyrProTyrAspGlyAlaAlaLeuLeuAlaGlyGlnArgPheAsp 40  
 TTGCGCATAGAAGCCTCCGAGCTGAAAGGCAATTTAAAGGCTTACCGCATCACCTGGAC  
 41 LeuArgIleGluAlaSerGluLeuLysGlyAsnLeuLysAlaTyrArgIleThrLeuAsp 60  
 GGCCAGCCTCTGGCGGGCCTCGAGCAAACCGCGCAGGGGGCCGGGCAGGCCGAGTGGACC  
 61 GlyGlnProLeuAlaGlyLeuGluGlnThrAlaGlnGlyAlaGlyGlnAlaGluTrpThr 80  
 CTGCGCGGTGCCTTCCTGCGCCCTGGAAGCCACCCCTCGAGGTCAGCCTCACCGACGAC  
 81 LeuArgGlyAlaPheLeuArgProGlySerHisThrLeuGluValSerLeuThrAspAsp 100  
 GCTGGGGAGAGCAGGAAGAGCGTACGTTGGGAGGCTCGGCAGAACCTTCGCTTGCCCCGA  
 101 AlaGlyGluSerArgLysSerValArgTrpGluAlaArgGlnAsnLeuArgLeuProArg 120  
 GCGGCCAAGAATGTGATTCTCTTCATTGGCGACGGGATGGGCTGGAACACCCTCAACGCC  
 121 AlaAlaLysAsnValIleLeuPheIleGlyAspGlyMetGlyTrpAsnThrLeuAsnAla 140  
 GCGCGCATCATCGCCAAAGGCTTTAACCCCGAAAACGGTATGCCCAACGGAAACCTCGAG  
 141 AlaArgIleIleAlaLysGlyPheAsnProGluAsnGlyMetProAsnGlyAsnLeuGlu 160  
 ATCGAGAGTGGTTACGTTGGGATGGCTACCGTCACTACCGGCAGCTTTGATAGCTTCATC  
 161 IleGluSerGlyTyrGlyGlyMetAlaThrValThrThrGlySerPheAspSerPheIle 180  
 GCGGACTCAGCTAACTCGGCTTCTTCCATCATGACCGGGCAGAAGGTGCAGGTGAATGCC  
 181 AlaAspSerAlaAsnSerAlaSerSerIleMetThrGlyGlnLysValGlnValAsnAla 200  
 CTCAACGTTTACCCATCAAACCTCAAAGATACCTGGCCTACCCCGGATCGAAACCTTA  
 201 LeuAsnValTyrProSerAsnLeuLysAspThrLeuAlaTyrProArgIleGluThrLeu 220  
 GCGGAGATGCTCAAGCGGGTACGCGGGGCCAGCATTGGGGTAGTGACCACCACCTTCGGC  
 221 AlaGluMetLeuLysArgValArgGlyAlaSerIleGlyValValThrThrThrPheGly 240  
 ACCGACGCTACCCCGGCTTCACTCAACGCCCCATACCGCCGCCGCGGTGATTACAGGCT  
 241 ThrAspAlaThrProAlaSerLeuAsnAlaHisThrArgArgArgGlyAspTyrGlnAla 260  
 ATCGCCGACATGTACTTTGGTAGAGGCGGGTTCGGTGTTCCTTGGATGTGATGCTCTTC  
 261 IleAlaAspMetTyrPheGlyArgGlyGlyPheGlyValProLeuAspValMetLeuPhe 280  
 GGTGGTTACGCGACTTCATCCCCAGAGCACCCCTGGCTCGCGGCGCAAGGATAGCACG  
 281 GlyGlySerArgAspPheIleProGlnSerThrProGlySerArgArgLysAspSerThr 300  
 GACTGGATTGCCGAATCCCAGAAGCTGGGCTACACCTTTGTCAGCACCCGAGCGAGCTG  
 301 AspTrpIleAlaGluSerGlnLysLeuGlyTyrThrPheValSerThrArgSerGluLeu 320  
 CTGGCGGCCAAACCCACCGATAAGCTGTTTGGGCTGTTCAACATTGACAACTTCCCCAGC  
 321 LeuAlaAlaLysProThrAspLysLeuPheGlyLeuPheAsnIleAspAsnPheProSer 340

[illegible]

Complete Gene Sequence (Part 2 of 2)

	TACCTAGACCGCCAGTGTGGAAAGCGGCCAGAGATGCTGGGAAGCTTTACCGATATGCC	
341	TyrLeuAspArgAlaValTrpLysArgProGluMetLeuGlySerPheThrAspMetPro	360
	TACCTCTGGGAGATGACCCAGAAAGCCGTGGAGGCTCTCTCCAGAAACGACAAAGGCTTT	
361	TyrLeuTrpGluMetThrGlnLysAlaValGluAlaLeuSerArgAsnAspLysGlyPhe	380
	TTCTTGATGGTTGAGGGGGGAATGGTGGATAAGTACGAGCACCCCTTGGACTGGCCCCGC	
381	PheLeuMetValGluGlyGlyMetValAspLysTyrGluHisProLeuAspTrpProArg	400
	GCACTTTGGGATGTACTCGAGCTGGACCGCGCGGTGGCTTGGGCCAAGGGCTATGCGGCC	
401	AlaLeuTrpAspValLeuGluLeuAspArgAlaValAlaTrpAlaLysGlyTyrAlaAla	420
	TCCACCCCGATACCCTGGTGATTGTACCGCCGACCACGCTCACTCGATCTCGGTGTTT	
421	SerHisProAspThrLeuValIleValThrAlaAspHisAlaHisSerIleSerValPhe	440
	GGCGGTTACGACTACTCCAAGCAGGCGCGGAGGGGTGGGGTTTATGAGGCCGCCAAG	
441	GlyGlyTyrAspTyrSerLysGlnGlyArgGluGlyValGlyValTyrGluAlaAlaLys	460
	TTCCCCACCTACGGCGACAAAAAGACGCCAACGGCTTTCCCTTGCCCCACCACTCGG	
461	PheProThrTyrGlyAspLysLysAspAlaAsnGlyPheProLeuProAspThrThrArg	480
	GGAATCGCGGTAGGCTTCGGGGCCACGCCGATTACTGTGAAACCTACCGGGCCCGCAG	
481	GlyIleAlaValGlyPheGlyAlaThrProAspTyrCysGluThrTyrArgGlyArgGlu	500
	GTCTACAAAGACCCACCATCTCCGACGGCAAAGGTGGTTACGTGGCCAACCTGAGGTC	
501	ValTyrLysAspProThrIleSerAspGlyLysGlyGlyTyrValAlaAsnProGluVal	520
	TGCAAGGAGCCGGGCCTTCCAACGTATCCGGCAACTCCAGTAGATAGCGCCAGGGCGTG	
521	CysLysGluProGlyLeuProThrTyrArgGlnLeuProValAspSerAlaGlnGlyVal	540
	CACACGGCTGATCCCATGCCGTGTTTGCCCTTGGCGTGGGTCTCAGTTCTTCAATGGC	
541	HisThrAlaAspProMetProLeuPheAlaPheGlyValGlySerGlnPhePheAsnGly	560
	CTCATCGACCAGACCGAGATCTTCTTCCGCATGGCCCAGGCCCTAGGGTTCAACCCCCAC	
561	LeuIleAspGlnThrGluIlePhePheArgMetAlaGlnAlaLeuGlyPheAsnProHis	580
	CTCAGAAGCCTTAA	
581	LeuGluLysProEnd	585

[illegible]

	ATGTATAAATGGATTATTGAGGGTAAGCTTGCCCCAAGCACCTTTTCCAAGCCTAGGTGAA	
1	MetTyrLysTrpIleIleGluGlyLysLeuAlaGlnAlaProPheProSerLeuGlyGlu	20
	CTAGCCGATCTCAAAAGACTTTTCGACGCCATTATTGTTCTTACAATGCCGCATGAACAA	
21	LeuAlaAspLeuLysArgLeuPheAspAlaIleIleValLeuThrMetProHisGluGln	40
	CCGCTTAATGAGAAATATATCGAGATATTAGAGAGCCATGGATTCCAAGTCCTCCATGTC	
41	ProLeuAsnGluLysTyrIleGluIleLeuGluSerHisGlyPheGlnValLeuHisVal	60
	CCCACGCTCGACTTTTCATCCTTTAGAAGCTTCGACCTTTTGAAAACAAGCATATTCATT	
61	ProThrLeuAspPheHisProLeuGluLeuPheAspLeuLeuLysThrSerIlePheIle	80
	GATGAAAACCTGGAGAGATCCACAGAGTGCTTGTCCTGTCATGGGAGGCATAGGCCGG	
81	AspGluAsnLeuGluArgSerHisArgValLeuValHisCysMetGlyGlyIleGlyArg	100
	AGCGGGCTTGTAAGTGTGCGTACTTAATATTCAAAGGTTATGATATTTACGACGCGGTA	
101	SerGlyLeuValThrAlaAlaTyrLeuIlePheLysGlyTyrAspIleTyrAspAlaVal	120
	AAGCATGTGAGAACGGTAGTGCCTGGTGCTATTGAAAACAGAGGGCAAGCGTTAATGCTT	
121	LysHisValArgThrValValProGlyAlaIleGluAsnArgGlyGlnAlaLeuMetLeu	140
	GAGAACTACTATACCCTGGTCAAAAGTTTCAACAGAGAGTTGCTGAGAGACTACGGGAAG	
141	GluAsnTyrTyrThrLeuValLysSerPheAsnArgGluLeuLeuArgAspTyrGlyLys	160
	AAAATTTTCACGCTCGGTGACCCGAAGGCGGTTCTCCACGCTTCTAAGACGACTCAGTTC	
161	LysIlePheThrLeuGlyAspProLysAlaValLeuHisAlaSerLysThrThrGlnPhe	180
	ACGATTGAACTCTTAAGCAACTTACACGTCAACGAGGCGTTTTCAATCAGTGCGATGGCT	
181	ThrIleGluLeuLeuSerAsnLeuHisValAsnGluAlaPheSerIleSerAlaMetAla	200
	CAATCACTGCTCCACTTTCACGACGTAAAGTCCGCTCTAAACTGAAAGAAGTATTCGAA	
201	GlnSerLeuLeuHisPheHisAspValLysValArgSerLysLeuLysGluValPheGlu	220
	AACATGGAATTCTCATCCGCCTCAGAGGAGGTTCTGTCATTTATTCACCTACTCGATTTT	
221	AsnMetGluPheSerSerAlaSerGluGluValLeuSerPheIleHisLeuLeuAspPhe	240
	TATCAGGATGGCAGGGTTGTTTTAACCATTTACGATTATCTCCCCGATAGGGTGGATTTG	
241	TyrGlnAspGlyArgValValLeuThrIleTyrAspTyrLeuProAspArgValAspLeu	260
	ATTTTATTGTGTAAGTGGGGTTGTGATAAAATAGTTGAAGTCTCGTCTTCAGCGAAGAAA	
261	IleLeuLeuCysLysTrpGlyCysAspLysIleValGluValSerSerSerAlaLysLys	280
	ACCGTTGAGAAGCTTGTAGGAAGAAAGGTTTCCCTATCTCGGGCTAATTACTTAGACTAT	
281	ThrValGluLysLeuValGlyArgLysValSerLeuSerTrpAlaAsnTyrLeuAspTyr	300
	GTTTAG	
301	ValEnd	302

Year	1913	1914	1915	1916	1917	1918	1919	1920	1921	1922	1923	1924	1925	1926	1927	1928	1929	1930	1931	1932	1933	1934	1935	1936	1937	1938	1939	1940	1941	1942	1943	1944	1945	1946	1947	1948	1949	1950	1951	1952	1953	1954	1955	1956	1957	1958	1959	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1913	1914	1915	1916	1917	1918	1919	1920	1921	1922	1923	1924	1925	1926	1927	1928	1929	1930	1931	1932	1933	1934	1935	1936	1937	1938	1939	1940	1941	1942	1943	1944	1945	1946	1947	1948	1949	1950	1951	1952	1953	1954	1955	1956	1957	1958	1959	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

1	ATGAGAATCCTCTCCACCAACGACGACGGCATCTATTCCAAACGGTCTGCGCGCGCGGGTG MetArgIleLeuLeuThrAsnAspAspGlyIleTyrSerAsnGlyLeuArgAlaAlaVal	20
21	AAGGGCCTGAGCGAGCTCGGCGAGGTCTACGTCGTCGCCCCGCTCTTCCAGAGGAGCGCG LysGlyLeuSerGluLeuGlyGluValTyrValValAlaProLeuPheGlnArgSerAla	40
41	AGCGGTCGGGCGATGACCCTACACAGGCCGATAAGGGCAAAGAGGGTTGACGTTCCCGGC SerGlyArgAlaMetThrLeuHisArgProIleArgAlaLysArgValAspValProGly	60
61	GCGAAGATAGCGTATGGCATAGACGGAACGCCGACCGACTGCGTGATTTTTGCCATCGCC AlaLysIleAlaTyrGlyIleAspGlyThrProThrAspCysValIlePheAlaIleAla	80
81	CGCTTCGGCGACTTTGATCTGGCGGTGACGGGATAAACCTAGGCGAGAACCTGAGCACG ArgPheGlyAspPheAspLeuAlaValSerGlyIleAsnLeuGlyGluAsnLeuSerThr	100
101	GAGATAACCGTCTCCGGAACGGCCTCGGCGGCGATAGAGGCTTCCACCCACGGGATTCCA GluIleThrValSerGlyThrAlaSerAlaAlaIleGluAlaSerThrHisGlyIlePro	120
121	AGTGTAGCTATAAGCCTCGAGGTCGAGTGAAGAAGACCTCGGCGAGGGGAGGGTATT SerValAlaIleSerLeuGluValGluTrpLysLysThrLeuGlyGluGlyGluGlyIle	140
141	GACTTCTCGGTTTTCAGCACACTTCCTGAGAAGGATAGCGACGGCTGTCCTTAAGAAGGGC AspPheSerValSerAlaHisPheLeuArgArgIleAlaThrAlaValLeuLysLysGly	160
161	CTGCCTGAAGGGGTGGACATGCTCAACGTGAACGTCCCTAGCGACGCCAGCGAGGGGACT LeuProGluGlyValAspMetLeuAsnValAsnValProSerAspAlaSerGluGlyThr	180
181	GAGATCGCCATAACGCGCCTCGCGAGGAAGCGCTATTCTCCGACGATAGAGGAGAGGATA GluIleAlaIleThrArgLeuAlaArgLysArgTyrSerProThrIleGluGluArgIle	200
201	GACCCCAAGGGCAACCCCTACTACTGGATCGTTGGCAGGCTCGTCCAGGAGTTTCGAGCCG AspProLysGlyAsnProTyrTyrTrpIleValGlyArgLeuValGlnGluPheGluPro	220
221	GGCACGGACGCCTACGCTCTGAAAGTCGAGAGAAAGGTCAGCGTCACGCCCATAAACATC GlyThrAspAlaTyrAlaLeuLysValGluArgLysValSerValThrProIleAsnIle	240
241	GACATGACTGCGAGGGTTGACTTTTGAGAACCTTCAAAGGCTTCTGAGCCTGTGA AspMetThrAlaArgValAspPheGluAsnLeuGlnArgLeuLeuSerLeuEnd	258

**Aquifex VF-5 Phosphatase (34A1A)**  
**Complete Gene Sequence**

1	ATGGAAGAACTTAAAAAAGTACCTAGAAAGTTGCAAAAATAGCCGCGCTCGCGGGTGGGCAG MetGluAsnLeuLysLysTyrLeuGluValAlaLysIleAlaAlaLeuAlaGlyGlyGln	20
21	GTTCTGAAAGAAAACCTTCGGAAAGGTAAAAAAGGAAAACATAGAGGAAAAAGGGGAAAAG ValLeuLysGluAsnPheGlyLysValLysLysGluAsnIleGluGluLysGlyGluLys	40
41	GACTTTGTAAAGTTACGTGGATAAAACTTCAGAGGAAAGGATAAAGGAGGTGATACTCAAG AspPheValSerTyrValAspLysThrSerGluGluArgIleLysGluValIleLeuLys	60
61	TTCTTTCCCGATCACGAGGTCGTAGGGGAAGAGATGGGTGCGGAGGGAAGCGGAAGCGAA PhePheProAspHisGluValValGlyGluGluMetGlyAlaGluGlySerGlySerGlu	80
81	TACAGGTGGTTTCATAGACCCCTTGACGGCACAAAGAACTACATAAACGGTTTTCCCATC TyrArgTrpPheIleAspProLeuAspGlyThrLysAsnTyrIleAsnGlyPheProIle	100
101	TTTGCCGTATCAGTGGGACTTGTTAAGGGAGAAGAGCCAATTGTGGGTGCGGTTTACCTT PheAlaValSerValGlyLeuValLysGlyGluGluProIleValGlyAlaValTyrLeu	120
121	CCTTACTTTGACAAGCTTTACTGGGGTGCTAAAGGTCTCGGGGCTTACGTAAACGGAAAG ProTyrPheAspLysLeuTyrTrpGlyAlaLysGlyLeuGlyAlaTyrValAsnGlyLys	140
141	AGGATAAAGGTAAAGGACAATGAGAGTTTAAAGCACGCCGGAGTGGTTTACGGATTTCCC ArgIleLysValLysAspAsnGluSerLeuLysHisAlaGlyValValTyrGlyPhePro	160
161	TCTAGGAGCAGGAGGGACATATCTATCTACTTGAACATATTCAAGGATGTCTTTTACGAA SerArgSerArgArgAspIleSerIleTyrLeuAsnIlePheLysAspValPheTyrGlu	180
181	GTTGGCTCTATGAGGAGACCCGGGGCTGCTGCGGTTGACCTCTGCATGGTGGCGGAAGGG ValGlySerMetArgArgProGlyAlaAlaAlaValAspLeuCysMetValAlaGluGly	200
201	ATATTTGACGGGATGATGGAGTTTGAATGAAGCCGTGGGACATAACCGCAGGGCTTGTA IlePheAspGlyMetMetGluPheGluMetLysProTrpAspIleThrAlaGlyLeuVal	220
221	ATACTGAAGGAAGCCGGGGGCGTTTACACACTTGTGGGAGAACCCTTCGGAGTTTTCGGAC IleLeuLysGluAlaGlyGlyValTyrThrLeuValGlyGluProPheGlyValSerAsp	240
241	ATAATTGCGGGCAACAAAGCCCTCCACGACTTTTATACTTCAGGTAGCCAAAAAGTATATG IleIleAlaGlyAsnLysAlaLeuHisAspPheIleLeuGlnValAlaLysLysTyrMet	260
261	GAAGTGGCGGTGTGA GluValAlaValEnd	265